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Ichthyophthirius multifillis.
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Eukaryochthirius multifillis
Eukaryocta' Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Ophryoglenina; Ichthyophthirius.

The bases 1 to 658)

Clark, T., Cordonnier-Pratt, M.-M., Sudman, M., Wentzel, V., Gingle, A.,
Dickerson, H., Lin, T.-L. and Pratt, L.H.
An EST database for Ichthyophthirius multifillis (G5 isolate)

Contact: Cordonnier-Pratt MM
The Unpublished (2002)

Contact: Cordonnier-Pratt MM
Taboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
FAX: 706 542 1860
FAX: 706 583 0210
Email: mmpratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector, and regions below Phred quality 16. The threshold for highest quality sequence
 B0134871 INITI_1_B
B0135036 INITI_2_D
B01345189 INITI_4_D
B0134985 INITI_4_D
B0134985 INITI_4_C
B0134810 INITI_4_C
B0134810 INITI_4_B
B0134905 INITI_4_B
B0135168 INITI_1_C
B0134799 INITI_2_D
B0134790 INITI_2_D
B0134790 INITI_2_D
B0134700 INITI_3_E
B0134761 INITI_3_E
B0134761 INITI_3_E
B013400 INITI_3_C
B0135114 INITI_3_C
B013640 INITI_3_C
B013640 INITI_3_C
B018691 Forbreadon
B018691 Tetracodon
AL439128 IT endo
B018691 Tetracodon
AL43619 Tetracodon
AL43662 Anopheles
B1285421 BJ285421
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AUTHORS
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BQ135164 INIT1_4_B
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                                                                                                                   ; Search time 1361.09 Seconds (without alignments)
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Copyright (c) 1993 - 2003 Compugen Ltd.
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    nucleic search, using sw model

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Listing first 45 summaries
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                                                                                                 /clone_lib="65" trophont cDNA (INITI)"
/clone_lib="65" trophont cDNA (INITI)"
/note="Vector: pBluescript SK(-) from Lambda Zap II;
Site_l: EcoRI; Site_2: EcoRI; The library was made from
trophont polyA+ RNA of the G5 parasite strain.

Double-stranded cDNA was linked to EcoRI adaptors, size
fractionated, and material >500 bp cloned into lambda ZAP
II. Plasmid DNA for sequencing was prepared by mass
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                                                                                                                                                                                                                                                                                   689 CITAAGGIGAAGCICCIGGCGIITAAGIITITGCIGGIGGIGCIGCCGCIGCAGGIGIIG 748
                                                                                                                                                                                                                                                                                                    AAGTATATGCTGAAGCTACTTAAAAAGCATAATGCGCCAGTTCCACTTTCGCAAAATTTT
                                                                                                                                                                                                                                                                                                                                   749 CIGCCGTIACTAGTTAATGTGTACCTTGCCAAATAAACAAAAAGGATTCTCCTGCCACTG
                                                                                                                                                                                                                                                                                                                                                  869 IICAAGACGGAGTGACACITGITITAGTAATTCAICCACATAATGTICITAATGCATTG
                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                        658;
                                                                                                                                                                                                                                      Score 404.4; DB 14; Length Pred. No. 1.3e-76;
                                                            1. .658
/cranism="Ichthyophthirius multifiliis"
/strain="65"
/db_xref="taxon:5932"
/db_xref="taxon-ort chwa (INII)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TATCGATTTCCTTATTATTTATTTCTTTCTATTATTG 1326
                                                                                                                                                                                                                                                               Mismatches 146;
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                    High quality sequence stop: 658
                                            Location/Qualifiers
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77.1%;
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                                                                                                                                                                                         excision."
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                                                                                                                                                                                                                                             Query Match
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BQ134912/c
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Inchryophthirius multifiliis.
Ichthyophthirius multifiliis.
Ichthyophthirius multifiliis.
Eukaryota: Alveolata: Ciliophora; Oligohymenophorea;
Hymenostomatida: Ophryoglenina; Ichthyophthirius.
I (bases 1 to 607)
Clark, T., Cordonnier-Pratt, M.-M., Sudman, M., Wentzel, V., Gingle, A.,
Dickerson, H., Lin, T.-L. and Pratt, L.H.
An EST database for Ichthyophthirius multifiliis (G5 isolate)
Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:5932"
/clone_lib="G5 trophont cDNA (INIT1)"
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/note="Vector: pBluescript SK(-) from Lambda Zap II:
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/note="Vector: pBluescript SK(-) from Lambda Zap II:
/note="Vector: pBluescript"
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/note: pBlu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    880 GIGACACTIGITITIAGTAAITCAICCACATAAIGITCITAAIGCAIIGCIAATIACIIT 939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 760 AGTTAATGTGTACCTTGCCAAATAAACAAAAACGATTCTCCTGCCACTGCAGGTGCCTAA 819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            820 GCTAAITITAGCCACATAAIGCAGIACTIAAIGICCAACIGGCACIGCAAITCAAGACGGA 879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271,
Tel: 705 542 1860
Fax: 706 583 0210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .;
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Pred. No. 2.1e-73;
0; Mismatches 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 193 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: mmpratt@uga.edu
Sequences have been trimmed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     104 g
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High quality sequence stop:
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300

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Ichthyophthirius multifilis.

Edwaryota's Alveolate; Cillophora; Oligohymenophorea;
Edwaryota; Alveolate; Cillophora; Oligohymenophorea;
Hymenostcomatida; Ophryoglenina; Ichthyophthirius.

S Clark'r. Cordonnier-Pratt,M.-M., Sudman,M., Wentzel,V., Gingle,A.,
Dickerson,H., Lin,T.-L. and Pratt,L.H.
An EST database for Ichthyophthirius multifiliis (G5 isolate)
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Fax: 706 542 1860
Email: mmprattleuga.edu
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/do.tore_lib="G5 trophont cDNA (INTI)"

/note="vector: pBluescript SK(-) from Lambda Zap II;

Site_l: EcoRI; Site_2: EcoRI; The library was made from trophont polyA+ RNA of the G5 parasite strain.

Double-stranded cDNA was linked to EcoRI adaptors, size fractionated, and material >500 bp cloned into lambda Zap II;

In Plasmid DNA for sequencing was prepared by mass
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequences have been trimmed to exclude PolyA, vector, and regions below Phred quality 16. The threshold for highest quality sequence
                                                                                                                                                                                                                            1109 CCGCAACTGAATGTACTAAATGTTCTGCTGGCTTTTTTGCATCAAAAACAACTGGTTTTA 1168
                                                                                                                                          1049 TGACCACATGTCCTGCTGGTACATGATGATGGAACATCAACTAATTTTGTAGCTT 1108
                                                                                                                                                                                                                                                                                                              1169 CAGCAGGTACTGATACATGTACTGAATGTACTAAAAATTAACTTCTGGTGCCACAGGTA 1228
                                                                                                                                                                                                                                                                                                                                                                                               1229 AAGTATATGCTGAAGCTACTCAAAAAGTATAATGCGCCTCCACTACTTTCGCTAAATTTT 1288
                   CTGGCTTTTACTAAAATAGTAATTTCGAAGCAGGTAAAAGTTAATGCAATAAGTGTGCAG 420
                                                                                                                                                                                                                                                  199 TAGCAAGTGAATGTACTAAATGTTAGGCTAACTTTTATGCATCAAAAACATCTGGTTTTG 240
                                                                                                                                                                                                                                                                                                                                 239 CAGCAGGTACTGATACATGTACTGAATGTTCTAAAAAATTAACTTCTGGTGCTACAGGTA 180
                                                                                                                                                                                                                                                                                                                                                                                                                          BQ135179 590 bp mRNA 11near EST 22-APP INTIL4_CO8.91_A006 G5 trophont cDNA (INIT1) Ichthyophthirius multifillis cDNA, mRNA sequence.
                                                                                                                                                                989 TAAGTAAAACTACTCCAGCACATGCTCCAGGTAATACTGCTACTTAAGCCACATAATGTT

    590
    /organism="Ichthyophthirius multifillis"

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High quality sequence stop: 590
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SOURCE
ORGANISM
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BQ135179/c
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                                                                                                                                                                                                                                                                                                BQ135164 602 bp mRNA linear EST 22-APR-2002 INITL4_B05.gl_A006 G5 trophont cDNA (INITL) Ichthyophthirius multifillis cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                 Ichthyophthirius multifillis.
Ichthyophthirius multifillis.
Ichthyophthirius multifillis.
Bukaryota, Alveolata; Cillophora; Oligohymenophorea;
Hymenostcmatida; Ophryoglenina; Ichthyophthirius.
I (bases 1 to 602)
Clark, T., Cordonnier-Pratt, M.-M., Sudman, M., Wentzel, V., Gingle, A., Dickerson, H., Lin, T.-L. and Pratt, L.H.
An EST database for Ichthyophthirius multifillis (G5 isolate)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strain="G5"

(db_xref="taxon:5932"

(db_xref="taxon:5932"

(dboe_lib="G5 trophont cDNA (INITI)"

// note="Vector: pBluescript SK(-) from Lambda Zap II;

// strain="tophont polyA+ RNA of the G5 parasite strain.

Double-stranded cDNA was linked to EcoRI adaptors, size fractionated, and material >500 bp cloned into lambda ZAP III. Plasmid DNA for sequencing was prepared by mass
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                                                         1240 GAAGCTACTCAAAAAGTATAATGCGCCTCCACTACTTTCGCTAAATTTTTATCGATTTCC 1299
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            809 CAGGICCCTAAGCIAATITAGCCACATAATGCAGTACTIAATGTCCAACIGGCACTGCAA 868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              869 ITCAAGACGGAGTGACACITGTTTTAGTAATTCATCCACATAATGTTCTTAATGCATTG 928
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism = "Ichthyophthirius multifiliis"
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High quality sequence start: 3
High quality sequence stop: 602
POLYA-Yes.
                                                                                                                                          1300 TTATTATTTATTTCTTTCTATTATTG 1326
                                                                                                                                                                   Location/Qualifiers
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BQ135164.1 GI:20261263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 706 542 1860
Fax: 706 583 0210
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                      187
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JOURNAL
COMMENT
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Gaps

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Length 502; Indels

Query Match

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INITL 4 E06.91_A006 G5 trophont cDNA (INIT) Ichthyophthirius multifiliis cDNA, mRNA sequence.
                            /strain="G5"
/db_xref="taxon:5932"
/db_xref="taxon:5932"
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/note="vector: pBluescript SR(-) from Lambda From
/rophont polyA+ RNA of the G5 parasaite Strain.
/polyA+ RNA of was linked to EcoRI adaptors, size
/ractionated, and material >500 bp cloned into lambda ZAP
// plasmid DNA for sequencing was prepared by mass
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Ichthyophthirius multifillis.
Ichthyophthirius multifillis
Bukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Ophryoglenina; Ichthyophthirius.
I (bases 1 to 6/5)
Clark,T., Cordonnier-Fratt,M.-M., Sudman,M., Wentzel,V., Ginglark,T., Lin,T.-L. and Pratt,L.H.
An Est database for Ichthyophthirius multifillis (G5 isolate)
Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Laboratory Commics and Bioinformatics
Laboratory of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
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        /organism="Ichthyophthirius multifiliis"
                                                                                                                                                                                                                                                                                                                       65;
                                                                                                                                                                                                                                                                                Score 317; DB 14;
Pred. No. 6.9e-58;
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84.6%;
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                                                               Gaps
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Contact: Condonier-Pratt MM
Laboratory for Genomics and BioInformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271,
Tel: 706 542 1860
Fax: 706 583 0210
                                                                                                   810 AGGIGCCTAAGCIAATITAGCCACATAATGCAGTACTTAATGICCAACTGGCACTGCAAT
                                                                                                                         870 TCAAGACGGAGTGACACTTGTTTTTAGTAATTCATCCACATAATGTTCTTAATGCATTGC
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0
                          DB 14; Length 590;
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Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Ophryoglenina; Ichthyophthirius.
1 (bases 1 to 502)
                                                               Indels
              Score 366.6; DB 14;
Pred. No. 1.6e-68;
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High quality sequence stop: 474
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Sequences have been trimmed
below Phred quality 16. The
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                                                                       Matches 423;
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RESULT 5 BQ134889/c LOCUS DEFINITION

ACCESSION VERSION KEYWORDS SOURCE

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          Fax: 706 583 0210
Email: mmpratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector, and regions
below Phred quality 16. The threshold for highest quality sequence
                                                                                                                                                             /db_xref="taxon:5932"
/clone_lib="65 trophont cDNA (INIT1)"
/note="Vector: pBluescript SK(-) from Lambda Zap II:
Site_l: EcoRI; Site_l: EcoRI; The library was made from
trophont potyA+ RNA of the G5 parasite strain.
Double-stranded cDNA was linked to EcoRI adaptors, size
fractionated, and material >500 bp cloned into lambda ZAP
excision."
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Pred. No. 8.1e-58;
0; Mismatches 164; Indels 34;
                                                                                                                                           /organism="Ichthyophthirius multifiliis"
/strain="G5"
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                                                                   Seq primer: T7
High quality sequence start: 42
High quality sequence stop: 675
POLYANO.
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Best Local Similarity 70.3%;
Matches 469; Conservative
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445 bp mRNA linear EST 22-APR-2002 mITI_1_B05.bl_A006 G5 trophont cDNA (INIT1) Ichthyophthirius B0134871
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Ichthyophthirius multifillis
Eukaryota, Alveolata; Ciliophora; Oligohymenophorea;
Bukaryota; Alveolata; Ciliophora; Oligohymenophorea;
I (bases 1 to 445)
Clark T., Cordonnier-Pratt, M.-M., Sudman, M., Wentzel, V., Gingle, A., Dickerson, H., Lin, T.-L. and Pratt, L.H.
Olickerson, H., Lin, T.-L. and Pratt, L.H.
Olichelished (2002)
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/note="Vector: pBluescript SK(-) from Lambda Zap II;
/note="Vector: pBluescript SK(-) from Lambda Zap II;
Stle_l: EcoRI; Stle_2: EcoRI; The library was made from
trophont polyA+ RNA of the G5 parasite Strain.
Double-stranded cDNA was linked to EcoRI adaptors, size
fractionated, and material >500 bp cloned into lambda ZAP
II. Plasmid DNA for sequencing was prepared by mass
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Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271,
Tel: 706 542 1860
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Pred. No. 5.4e-56;
0; Mismatches 68; Indels 0;
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/db_xref="taxon:5932"
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EST.
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83.7%;
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Matches 437;
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JOURNAL
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BQ135189
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KEYWORDS
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An EST database for Ichthyophthirius multifiliis (G5 isolate)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db xref="taxon:5932"
/db xref="taxon:5932"
/clone_lib="G5 trophont cDNA (INIT1)"
/clone_lbe="G5 trophont cDNA (INIT1)"
/clone_lbe="Cort: pRluescript SK(-) from Lambda Zap II;
/clone_vector: pRluescript SK(-) from Lambda Zap II;
/clone_vector: pRluescript SK(-) from Lambda Zap II;
/clone trophont polyA+ RNA of the G5 parasite strain.
/clone trophont polyA+ RNA of the G5 parasite strain.
/clone trophont polyA+ RNA of was an inked to Ecorl adaptors, size fractionated, and material >500 bp cloned into lambda ZAP II. Plasmid DNA for sequencing was prepared by mass
                                                                                                                                                                                                                                                                                       EST 22-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: mmpratt@uga.edu Sequences have been trimmed to exclude PolyA, vector, and regions below phred quality 16. The threshold for highest quality sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1003 CCAGCACATGCTCCAGGTAATACTGCTACTTAAGCCACATAATGTTTGACCACATGTCCT 1062
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                                                                      297
1146 TGCATCAAAAACAACTGGTTTTACAGCAGGTACTGATACATGTACTGAATGTACTAAAAA 1205
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The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
                                                                                                                                                                                                                                                                                     BQ135036 419 bp mRNA linear EST 22-API INTTL_2_D10.gl_A006 G5 trophont cDNA (INITL) Ichthyophthirius multifillis cDNA, mRNA sequence.
                                                                                                                                                  356 TCAGCATCTGTTCCAGGTAATAGTGCTACTTCAGCCACATAATGTTAAAACGATTGCCCT
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Ichthyophthirius multifiliis
Eukaryota, Alveolata, Ciliophora; Oligohymenophorea;
Hymenostomatida; Ophryoglenina; Ichthyophthirius.
(bases 1 to 419)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22.2%; Score 294.4; DB 14;
85.4%; Pred. No. 4.9e-53;
ive 0; Mismatches 56;
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High quality sequence stop: 419
POLYA-Yes.
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Contact: Cordonnier-Pratt MM
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74 c
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Matches 328; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 706 542 1860
Fax: 706 583 0210
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Ichthyophthirius multifiliis.
Ichthyophthirius multifiliis
Bukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Bukaryota; Alveolata; Ciliophora; Ichthyophthirius.

1 (bases 1 to 661)
Clark, T., Cordonniar-Pratt, M.-M., Sudman, M., Wentzel, V., Gingle, A.,
Dickerson, H., Lin, T.-L. and Pratt, L.H.
An EST database for Ichthyophthirius multifiliis (G5 isolate)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              EST 22-APR-2002
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The University of Georgia, Department of Plant Biology
The University of Georgia, Department of Plant Biology
The University of Georgia, Department of Plant Biology
Tell: 706 542 1860
Fax: 706 583 0210
Fax: 706 583 0210
Fax: 706 been trimmed to exclude PolyA, vector, and regions
Sequences have been trimmed to exclude PolyA, vector, and regions
below Phred quality 16. The threshold for highest quality sequence
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                                                                                                                                                                  176 CCATGTACTGAATGTTTTAAAAAATTAACTTCCGGTGCTACACGTAAAGTATACGCGGAA 117
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BQ135189
ACTAAATGTTCTGCTGGCTTTTTTGCATCAAAAACAACTGGTTTTACAGCAGGTACTGAT
                                                                                 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21.2%; Score 280.6; DB 14; Length 661; 66.3%; Pred. No. 4.2e-50; ive 0; Mismatches 189; Indels 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Ichthyophthirius multifiliis"
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High quality sequence stop: 6
POLYA-No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (2002)
Contact: Cordonnier-Pratt MM
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1155 AAC 1157
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AUTHORS
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                                                                          480
                                                                                                                                                                                                                                                                                                                                          TGCCAAATAAACAAAAACGATTCTCCTGCCACTGCAGGTGCCTAAGCTAATTTAGCCACA 834
                                                                                                                                                                                                                                                                                                                              AGTAATTCATCCACATAATGTTCTTAATGCATTGCTAATTACTTTTTTAATGGTAATTTC 954
                                                                                                                                                                                                                                                                                                                                                                                   GATCTTGCTAATAATCCTGAAGTTCCTAATGTTTCTAGCCCTAATGGTTAATGCGTAGCT 60
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Ichthyophthirius multifillis.
Ichthyophthirius multifillis
Eukaryota; Alveolata; Cillophora; Oligohymenophorea;
Hymenostomatida; Ophryoglenina; Ichthyophthirius.
I (bases I to 599)
Clark,T., Cordonnier-Pratt,M.-M., Sudman,M., Wentzel,V., Ging.
Dickerson,H., Lin,T.-L. and Pratt,L.H.
An EST database for Ichthyophthirius multifillis (G5 isolate)
                                                               TAATGTAGCAATTAATGTCCTACTGGCACTGTACTTGATGATGGAGTGACACTTGTTTTT
                                                                                                         AATACATCAGCCACATTATGTGTTAAATGCAGACCTAACTTTTACTATAATGGTGGTTCT
                                                                                                                      GTTTTTGCTGCTGCTGCTGCTGCAGGTGTTGCTGCCGTTACTAGTTAATGTGTACCT
                                                                                                                                                                                                                                                                                    TAATGCAGTACTTAATGTCCAACTGCACTGCAATTCAAGACGGAGTGACACTTGTTTT
                                                                                                                                                                                                                                                                                                Unpublished (2002)
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271,
Tel: 706 542 1860
Email: mmpratt@uga.edu
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High quality sequence stop: 506
POLYA-No.
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BQ134821.1 GI:20260920
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BQ134821/c
LOCUS
DEFINITION
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                     508
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JOURNAL
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KEYWORDS
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/organism="Ichthyophthirius multifillis"
/strain="G5"
/db_xxef="taxon:5932"
/clone_lib="d5 trophont cDNA (INITI)"
/note="Vector: pBluescript SK(-) from Lambda Zap II;
/note="vector: pBluescript SK(-) from Lambda Zap II;
Site_1: EcoRI; Site_2: EcoRI; The library was made from trophont polyA+ RNA of the G5 parasite strain.
Double-stranded cDNA was linked to EcoRI adaptors, size fractionated, and material >500 bp cloned into lambda ZAP II. Plasmid DNA for sequencing was prepared by mass exclaion.
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Ichthyophthirius multifiliis.
Ichthyophthirius multifiliis.
Eukaryota: Alveolata: Ciliophora; Oligohymenophorea;
Hymenostomatida: Ophryoglenina; Ichthyophthirius.
1 (bases 1 to 592)
Clark, T., Cordonnier-Pratt, M.-M., Sudman, M., Wentzel, V., Gingle, A.,
Dickerson, H., Lin, T.-L. and Pratt, L.H.
An EST database for Ichthyophthirius multifillis (G5 isolate)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mRNA linear EST 22-APR-2002 CDNA (INIT1) IChthyophthirius
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TAATTTTGTAGCTTCCGCAACTGAATGTACTAAATGTTCTGCTGGCTTTTTTGCATCAAA 1154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          194 CAATAAGTGTGCAGTAAATTAAAACTGGTTCAGCATCTGTTCCAGGTAATAGTGCTACTTC 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGCCACATAATGTTTGACCACATGTCCTGCTGGTACAGTACTTGATGATGGAACATCAAC 1094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      675 TAATGGTGGTTCTCCTTAAGGTGAAGCTCCTGGCGTTTAAGTTTTTGCTGCTGGTGCTGC 734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             434 AATTCCTATGGTTCCTGGCCCTAATAGTAAATGCGTAGCTTGCGAATCAAAAAAGACCAA 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     854
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                                                                                                                                                                                                                                                                                                                                                                           Score 263.8; DB 14; Length 599; Pred. No. 1.7e-46;
                                                                                                                                                                                                                                                                                                    1 others
                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 1.7e-46;
0; Mismatches 137; Indels
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multifilis cDNA, mRNA BQ134985
BQ134985.1 GI:20261084
                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 71.6%;
Matches 346; Conservative
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POLYA=No.
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Matches 320;
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ORIGIN
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ORGANISM
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                                                                                                        DEFINITION
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JOURNAL
                                                                                                                                                         ACCESSION
                                                                                                                                                                             VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                           REFERENCE
                                       RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:5932"
/clone_lib="65 trophont cDNA (INIT1)"
/note="Vector: pBluescript SK(*) from Lambda Zap II;
/note="Vector: pBluescript" from Lambda Loon Loon Lambda La
                                                                                                                                                                                Sequences have been trimmed to exclude PolyA, vector, and regions below Phred quality 16. The threshold for highest quality sequence is 20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  486
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            899
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  608
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              549 CTAAGCTAATTTAGCCACATAATGTAGCAATTAATGTCCTACTGGCACTGTACTTGATGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGGAGTGACACTTGTTTTAATACATCAGCCACATTATGTGTTAAATGCAGACCTAACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         669 TTACTATAATGGTGGTTCTCCTTAAGGTGAAGCTCCTGGCGTTTAA---------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --GTTTTTGCTGCTGCTGCCGCTGCAGGTGTTGCTGCCGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          127 CGGAGCAATATTTATTATTATTATCAATCTCATAATGTACTTTTTGTAAAGTTGACTT
                                Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271,
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@uga.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 592;
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                                                                                                                                                                                                                                                                                                                                                                /organism="Ichthyophthirius multifillis"
/strain="G5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18.8%; Score 249.2; DB 14; 66.6%; Pred. No. 2.3e-43; ive 0; Mismatches 163;
                                                                                                                                                                                                                                                                                   quality sequence stop: 575
                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                        Cordonnier-Pratt MM
                                                                                                                                                                                                                                                             Seq primer: JEN REV
High quality sequence
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Unpublished (2002)
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COMMENT
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538 bp mRNA linear EST 22-APR-2002 trophont cDNA (INIT1) Ichthyophthirius
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/note="vector: pBluescript SK(-) from Lambda Zap II:
Site_1: EcoRI; Site_2: EcoRI; The library was made from
trophont polyA+ RNA of the G5 parasite strain.
Double-stranded cDNA was linked to EcoRI adaptors, size
fractionated, and material >500 bp cloned into lambda ZAP
II. plasmid DNA for sequencing was prepared by mass
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gingle, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sednence
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                                                                                                                                                                                                                                                          Inchthyophthirius multifiliis.
Ichthyophthirius multifiliis.
Ichthyophthirius multifiliis
Eukaryota; Alveclata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Ophryoglenina; Ichthyophthirius.
I (bases 1 to 538)
Clark T., Cordonnier-Pratt, M.-M., Sudman, M., Wentzel, V., Ginglark T., Cordonnier-Pratt, M.-M., Sudman, M., Wentzel, V., Ginglan EST database for Ichthyophthirius multifiliis (G5 isolate)
Unpublished (2002)
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Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
The University of Georgia, Department of Plant Biology
The Table Search Search
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Pred. No. 1.4e-41;
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/db_xref="taxon:5932"
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                                                                                                                                                                                             BQ134810.1 GI:20260909
                                                        INITI_4_C08.bl_A006 G5 multifiliis cDNA, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: mmpratt@uga.edu
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illarity 70.8%;
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Seq primer: JEN REV
High quality sequenc
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Inchtyophthirius multifiliis.
Eukaryota, Alveolata (Lilophora; Oligohymenophorea;
Eukaryota, Alveolata (Lilophora; Oligohymenophorea;
Hymenostomatida; Ophryoglenina; Ichthyophthirius.

(Lark, T., Cordonnier-Pratt, M.-M., Sudman, M., Wentzel, V., Gingle, A.,
Dickerson, H., Lin, T.-L. and Pratt, L.H.
An EST database for Ichthyophthirius multifiliis (G5 isolate)
Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:5932"
/clone_lib="65 trophont cDNA (INITI)"
/note="Vector: pBluescript SK(-) from Lambda Zap II;
/site_l: EcoRI; Site_2: EcoRI; The library was made from trophont polyA+ RNA of the 65 parasite strain.

Double-stranded cDNA was linked to EcoRI adaptors, size fractionated, and material >500 bp cloned into lambda Zap II. Plasmid DNA for sequencing was prepared by mass
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                                             AGCCACATAATGTTTGACCACATGTCCTGCTGGTACAGTACTTGATGAAGAACATCAAC 1094
USA
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Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271,
Tel: 706 542 1860
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    631
    /organism="Ichthyophthirius multifiliis"
/strain="G5"

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                                                                                                       1095 TAATTTTGTAGCTTCCGCAACTGAATGTACTA 1126
                                                                                                                          506 TAATTTGTAGCTTTAGCAAGTGAATGTACTA 537
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High quality sequence stop: 630
POLYA-No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: mmpratt@uga.edu
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Best Local Similarity 65.8 Matches 415; Conservative
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BQ134827
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HQ134905 630 bp mRNA linear EST 22-APR-2002 INITL_LF04.bl_A006 G5 trophont cDNA (INITL) Ichthyophthirius mullifililis cDNA, mRNA sequence.
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/note="Vector: pBluescript SK(-) from Lambda 2ap II;
Site_l: EcoRI; Site_2: EcoRI; The library was made from
trophont polyA+ RNA of the G5 parasite strain.
186 TAATGGTAATTAACCTTTCGCAGCAAATAATGCTGCTAGAGGTATATGTGTACCATGCCA 245
                                                                                                          512
                                                                                                                                                                             365
                                                                                                                                                                                                                                                        ATCAGCCGCATAATGTGTTAAATGCAAACCTAACTTTTACTATAATGGTGGTTCTCCTTA 425
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The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271,
Tel: 706 542 1860
Fax: 706 583 0210
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Ichthyophthirius multifillis
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida: Ophryoglenina; Ichthyophthirius.
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High quality sequence stop: 629
POLYA-No.
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/db_xref="taxon:5932"
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regions sequence

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/db_xref="taxon:5932"
/clone_lib="65 trophont cDNA (INIT1)"
/note="vector: pBluescript SK(-) from Lambda Zap II;
/note="vector: pBluescript SK(-) from Lambda Zap II;
/note="vector: pBluescript SK(-) from Lambda made from Sile_1: EcoRI; Site_2: EcoRI; The library was made from Sile_1: EcoRI; Site_4: Site_4: Sile_4: Strain poly4+ RNA of the G5 parasite strain.
/noble-stranded cDNA was linked to EcoRI adaptors, size fractionated, and material >500 bp cloned into lambda ZAP fire the sequencing was prepared by mass excision."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   359 GATTGCAAATCCTGATCTTGCTAATAATCCTGAAGTTCCTAATGTTTCTAGCCCTAATGG 418
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11 AGGAGCTGCAGATATATACTTGTACTCATTGCTAAAAACACTTTTACTTTAATGGTGG 70
                   Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
TT: 706 542 1860
Fax: 706 583 0210
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                                                                                          Email: mmpratt@uga.edu
Email: mmpratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector, and
below Phred quality 16. The threshold for highest quality
is 20.
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0; Mismatches
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                                                                                                                                                                                              Seq primer: T7
High quality sequence start:
High quality sequence stop: 6
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           Contact: Cordonnier-Pratt MM
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62.68;
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Clark,T., Cordonnier-Pratt,M.-M., Sudman,M., Wentzel,V., Gingle,A.,
Clark,T., Lin,T.-L. and Pratt,L.H.
An EST database for Ichthyophthirius multifillis (G5 isolate)
Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EST 22-APR-2002
                                                                                                                                                                                    3,
Louble-Stranded CDNA was linked to EcoRI adaptors, size fractionated, and material >500 bp cloned into lambda ZAP II. Plasmid DNA for sequencing was prepared by mass excision."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 509 GCCAACTAAACAAAACGATTCTCCTGCCACTGCAGGTGCCTAAGCTAATTTAGCCACAl 568
                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAGCTAATGGTAATTAACCTTTCGCAGCAAATAATGCTGCTAGAGGTATATGTGTACCAT 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  362 ATAGATCAGCCGCATAATGTGTTAAATGCAAACCTAACTTTTACTATAATGGTGGTTCTC 421
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                                                                                                                                                                                                                                                                                                                                                                                                 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BQ135168 687 bp mRNA linear EST 22-API INITL4_B09.gl_A006 G5 trophont cDNA (INITL) Ichthyophthirius multifillis cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                 62 TICCATGICCIGAIGGIACTIAGACICAAGCIGGAITGACIGAIGIAGGIGCIGCIGAIC 121
                                                                                                                                                                                      45; Gaps
                                                                                                                                                                                                                          61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    475 ATCTTGCTAATAATCCTGAAGTTCCTAATGTTTCTAGCCCTAATGGTTAATGCGTAGCTT
                                                                                                                                                                                                                                                 242 GCCAAATAAACAGAGTAGGCTCTGTTACCAATGCAGGTGACTTAGCTACTTTAGCCACAT
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                                                                                                                                                                                                                        2 IGAAAIATAAATTTTATTAATTTTAATTTTCTTTATTATTAATGAATTAAGGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       187 AGGCTCCTGGTGCTGTACAATTC-----AATCCAGGTGTTAGTCAGTGCATAGCTT
                                                                                                                                                 Length 630;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ichthyophthirius multifiliis.
Ichthyophthirius multifiliis
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Ophryoglenina; Ichthyophthirius.
                                                                                                                                                                                      Indels
                                                                                                                                               Score 236.6; DB 14;
Pred. No. 1.1e-40;
0; Mismatches 174; 1
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DEFINITION
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